

PCT

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/673,198

DATE: 12/26/2000  
 TIME: 13:19:35

Input Set : A:\1241.16 sequence.txt  
 Output Set: N:\CRF3\12262000\I673198.raw

2 <110> APPLICANT: NIYAKE, Koichiro; HASHIMOTO, Shinichi; MOTOYAMA Hiroaki;  
 3 OZAKI, Akio; SETO, Haruo; KUZAYAMA, Tomohisa; TAKAHASHI, Shunji  
 5 <120> TITLE OF INVENTION: A process for producing isoprenoid compounds by  
 6 microorganisms and a method for screening compounds with  
 7 antibiotic or weeding activity  
 W--> 9 <130> FILE REFERENCE:  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/673,198  
 C--> 12 <141> CURRENT FILING DATE: 2000-10-12  
 14 <150> PRIOR APPLICATION NUMBER: JP98/103101  
 15 <151> PRIOR FILING DATE: 1998-04-14  
 17 <150> PRIOR APPLICATION NUMBER: JP98/221910  
 18 <151> PRIOR FILING DATE: 1998-08-05  
 20 <150> PRIOR APPLICATION NUMBER: JP99/035739  
 21 <151> PRIOR FILING DATE: 1999-02-15  
 23 <160> NUMBER OF SEQ ID NOS: 34  
 25 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply  
 Corrected Diskette Needed

BEST AVAILABLE COPY

ERRORED SEQUENCES

392 <210> SEQ ID NO: 6  
 393 <211> LENGTH: 1860  
 394 <212> TYPE: DNA  
 395 <213> ORGANISM: Escherichia coli  
 397 <220> FEATURE:  
 398 <221> NAME/KEY: CDS  
 399 <222> LOCATION: (1)..(1860)  
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 403 48  
 405 Met Ser Phe Asp Ile Ala Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser  
 406 1 5 10 15  
 E--> 408 acc cag gag tta cga ctg ttg ccg aaa gag agt tta ccg aaa ctc tgc  
 409 96  
 411 Thr Gln Glu Leu Arg Leu Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys  
 412 20 25 30  
 E--> 414 gac gaa ctg cgc cgc tat tta ctc gac agc gtg agc cgt tcc agc ggg  
 415 144  
 417 Asp Glu Leu Arg Arg Tyr Leu Leu Asp Ser Val Ser Arg Ser Ser Gly  
 418 35 40 45  
 E--> 420 cac ttc gcc tcc ggg ctg ggc acg gtc gaa ctg acc gtg gcg ctg cac  
 421 192  
 423 His Phe Ala Ser Gly Leu Gly Thr Val Glu Leu Thr Val Ala Leu His  
 424 50 55 60  
 E--> 426 tat gtc tac aac acc ccg ttt gac caa ttg att tgg gat gtg ggg cat  
 427 240  
 429 Tyr Val Tyr Asn Thr Pro Phe Asp Gln Leu Ile Trp Asp Val Gly His

format error  
 48

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430 65 70 75 80  
E--> 432 cag gct tat ccg cat aaa att ttg acc gga cgc cgc gac aaa atc ggc  
433 288  
435 Gln Ala Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly  
436 85 90 95  
E--> 438 acc atc cgt cag aaa ggc ggt ctg cac ccg ttc ccg tgg cgc ggc gaa  
439 336  
441 Thr Ile Arg Gln Lys Gly Gly Leu His Pro Phe Pro Trp Arg Gly Glu  
442 100 105 110  
E--> 444 agc gaa tat gac gta tta agc gtc ggg cat tca tca acc tcc atc agt  
445 384  
447 Ser Glu Tyr Asp Val Leu Ser Val Gly His Ser Ser Thr Ser Ile Ser  
448 115 120 125  
E--> 450 gcc gga att ggt att gcg gtt gct gcc gaa aaa gaa ggc aaa aat cgc  
451 432  
453 Ala Gly Ile Gly Ile Ala Val Ala Ala Glu Lys Glu Gly Lys Asn Arg  
454 130 135 140  
E--> 456 cgc acc gtc tgt gtc att ggc gat ggc gcg att acc gca ggc atg gcy  
457 480  
459 Arg Thr Val Cys Val Ile Gly Asp Gly Ala Ile Thr Ala Gly Met Ala  
460 145 150 155 160  
E--> 462 ttt gaa gcg atg aat cac gcg ggc gat atc cgt cct gat atg ctg gtg  
463 528  
465 Phe Glu Ala Met Asn His Ala Gly Asp Ile Arg Pro Asp Met Leu Val  
466 165 170 175  
E--> 468 att ctc aac gac aat gaa atg tgc att tcc gaa aat gtc ggc gcg ctc  
469 576  
471 Ile Leu Asn Asp Asn Glu Met Ser Ile Ser Glu Asn Val Gly Ala Leu  
472 180 185 190  
E--> 474 aac aac cat ctg gca cag ctg ctt tcc ggt aag ctt tac tct tca ctg  
475 624  
477 Asn Asn His Leu Ala Gln Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu  
478 195 200 205  
E--> 480 cgc gaa ggc ggg aaa aaa gtt ttc tct ggc gtg ccc cca att aaa gag  
481 672  
483 Arg Glu Gly Gly Lys Lys Val Phe Ser Gly Val Pro Pro Ile Lys Glu  
484 210 215 220  
E--> 486 ctg ctc aaa cgc acc gaa gaa cat att aaa ggc atg gta gtg cct ggc  
487 720  
489 Leu Leu Lys Arg Thr Glu Glu His Ile Lys Gly Met Val Val Pro Gly  
490 225 230 235 240  
E--> 492 acg ttg ttt gaa gag ctg ggc ttt aac tac atc ggc ccc gtg gac ggt  
493 768  
495 Thr Leu Phe Glu Glu Leu Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly  
496 245 250 255  
E--> 498 cac gat gtg ctg ggg ctt atc acc acg cta aag aac atg cgc gac ctg  
499 816  
501 His Asp Val Leu Gly Leu Ile Thr Thr Leu Lys Asn Met Arg Asp Leu  
502 260 265 270

*Janne*

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E--> 504 aaa ggc ccg cag ttc ctg cat atc atg acc aaa aaa ggt cgt ggt tat  
 505 864  
 507 Lys Gly Pro Gln Phe Leu His Ile Met Thr Lys Lys Gly Arg Gly Tyr  
 508 275 280 285  
 E--> 510 gaa ccg gca gaa aaa gac ccg atc act ttc cac gcc gtg cct aaa ttt  
 511 912  
 513 Glu Pro Ala Glu Lys Asp Pro Ile Thr Phe His Ala Val Pro Lys Phe  
 514 290 295 300  
 E--> 516 gat ccc tcc agc ggt tgt ttc ccg aaa agt agc ggc ggt ttg ccg agc  
 517 960  
 519 Asp Pro Ser Ser Gly Cys Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser  
 520 305 310 315 320  
 E--> 522 tat tca aaa atc ttt ggc gac tgg ttg tgc gaa acg gca gcg aaa gac  
 523 1008  
 525 Tyr Ser Lys Ile Phe Gly Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp  
 526 325 330 335  
 E--> 528 aac aag ctg atg gcg att act ccg gcg atg cgt gaa ggt tcc ggc atg  
 529 1056  
 531 Asn Lys Leu Met Ala Ile Thr Pro Ala Met Arg Glu Gly Ser Gly Met  
 532 340 345 350  
 E--> 534 gtc gag ttt tca cgt aaa ttc ccg gat cgc tac ttc gac gtg gca att  
 535 1104  
 537 Val Glu Phe Ser Arg Lys Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile  
 538 355 360 365  
 E--> 540 gcc gag caa cac gcg gtg acc ttt gct gcg ggt ctg gcg att ggt ggg  
 541 1152  
 543 Ala Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly  
 544 370 375 380  
 E--> 546 tac aaa ccc att gtc gcg att tac tcc act ttc ctg caa cgc gec tat  
 547 1200  
 549 Tyr Lys Pro Ile Val Ala Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr  
 550 385 390 395 400  
 E--> 552 gat cag gtg ctg cat gac gtg gcg att caa aag ctt ccg gtc ctg ttc  
 553 1248  
 555 Asp Gln Val Leu His Asp Val Ala Ile Gln Lys Leu Pro Val Leu Phe  
 556 405 410 415  
 E--> 558 gcc atc gac cgc gcg ggc att gtt ggt gct gac ggt caa acc cat cag  
 559 1296  
 561 Ala Ile Asp Arg Ala Gly Ile Val Gly Ala Asp Gly Gln Thr His Gln  
 562 420 425 430  
 E--> 564 ggt gct ttt gat ctc tct tac ctg cgc tgc ata ccg gaa atg gtc att  
 565 1344  
 567 Gly Ala Phe Asp Leu Ser Tyr Leu Arg Cys Ile Pro Glu Met Val Ile  
 568 435 440 445  
 E--> 570 atg acc ccg agc gat gaa aac gaa tgt cgc cag atg ctc tat acc ggc  
 571 1392  
 573 Met Thr Pro Ser Asp Glu Asn Glu Cys Arg Gln Met Leu Tyr Thr Gly  
 574 450 455 460  
 E--> 576 tat cac tat aac gat ggc ccg tca gcg gtg cgc tac ccg cgt ggc aac

*Janne*

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577 1440  
579 Tyr His Tyr Asn Asp Gly Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn  
580 465 470 475 480  
E--> 582 gcg gtc ggc gtg gaa ctg acg ccg ctg gaa aaa cta cca att ggc aaa  
583 1488  
585 Ala Val Gly Val Glu Leu Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys  
586 485 490 495  
E--> 588 ggc att gtg aag cgt cgt ggc gag aaa ctg gcg atc ctt aac ttt ggt  
589 1536  
591 Gly Ile Val Lys Arg Arg Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly  
592 500 505 510  
E--> 594 acg ctg atg cca gaa gcg gcg aaa gtc gcc gaa tcg ctg aac gcc acg  
595 1584  
597 Thr Leu Met Pro Glu Ala Ala Lys Val Ala Glu Ser Leu Asn Ala Thr  
598 515 520 525  
E--> 600 ctg gtc gat atg cgt ttt gtg aaa ccg ctt gat gaa gcg tta att ctg  
601 1632  
603 Leu Val Asp Met Arg Phe Val Lys Pro Leu Asp Glu Ala Leu Ile Leu  
604 530 535 540  
E--> 606 gaa atg gcc gcc agc cat gaa gcg ctg gtc acc gta gaa gaa aac gcc  
607 1680  
609 Glu Met Ala Ala Ser His Glu Ala Leu Val Thr Val Glu Glu Asn Ala  
610 545 550 555 560  
E--> 612 att atg ggc ggc gca ggc agc ggc gtc aac gaa gtc ctg atg gcc cat  
613 1728  
615 Ile Met Gly Gly Ala Gly Ser Gly Val Asn Glu Val Leu Met Ala His  
616 565 570 575  
E--> 618 cgt aaa cca gta ccc gtg ctg aac att ggc ctg ccg gac ttc ttt att  
619 1776  
621 Arg Lys Pro Val Pro Val Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile  
622 580 585 590  
E--> 624 ccg caa gga act cag gaa gaa atg cgc gcc gaa ctc ggc ctc gat gcc  
625 1824  
627 Pro Gln Gly Thr Gln Glu Glu Met Arg Ala Glu Leu Gly Leu Asp Ala  
628 595 600 605  
E--> 630 gct ggt atg gaa gcc aaa atc aag gcc tgg ctg gca  
631 1860  
633 Ala Gly Met Glu Ala Lys Ile Lys Ala Trp Leu Ala  
634 610 615 620  
637 <210> SEQ ID NO: 7  
638 <211> LENGTH: 897  
639 <212> TYPE: DNA  
640 <213> ORGANISM: Escherichia coli  
642 <220> FEATURE:  
643 <221> NAME/KEY: CDS  
644 <222> LOCATION: (1)..(897)  
646 <400> SEQUENCE: 7  
E--> 647 atg gac ttt ccg cag caa ctc gaa gcc tgc gtt aag cag gcc aac cag  
648 48

*Danne*

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650 Met Asp Phe Pro Gln Gln Leu Glu Ala Cys Val Lys Gln Ala Asn Gln  
651 1 5 10 15  
E--> 653 gcg ctg agc cgt ttt atc gcc cca ctg ccc ttt cag aac act ccc gtg  
654 96  
655 Ala Leu Ser Arg Phe Ile Ala Pro Leu Pro Phe Gln Asn Thr Pro Val  
657 20 25 30  
E--> 659 gtc gaa acc atg cag tat ggc gca tta tta ggt ggt aag cgc ctg cga  
660 144  
662 Val Glu Thr Met Gln Tyr Gly Ala Leu Leu Gly Gly Lys Arg Leu Arg  
663 35 40 45  
E--> 665 cct ttc ctg gtt tat gcc acc ggt cat atg ttc ggc gtt agc aca aac  
666 192  
668 Pro Phe Leu Val Tyr Ala Thr Gly His Met Phe Gly Val Ser Thr Asn  
669 50 55 60  
E--> 671 acg ctg gac gca ccc gct gcc gcc gtt gag tgc tgc gtc gtt tac tca  
672 240  
674 Thr Leu Asp Ala Pro Ala Ala Val Glu Cys Ile His Ala Tyr Ser  
675 65 70 75 80  
E--> 677 tta att cat gat gat tta ccg gca atg gat gat gac gat ctg cgt cgc  
678 288  
680 Leu Ile His Asp Asp Leu Pro Ala Met Asp Asp Asp Asp Leu Arg Arg  
681 85 90 95  
E--> 683 ggt ttg cca acc tgc cat gtg aag ttt ggc gaa gca aac gcg att ctc  
684 336  
686 Gly Leu Pro Thr Cys His Val Lys Phe Gly Glu Ala Asn Ala Ile Leu  
687 100 105 110  
E--> 689 gct ggc gac gct tta caa acg ctg cgc ttc tcg att tta agc gat gcc  
690 384  
692 Ala Gly Asp Ala Leu Gln Thr Leu Ala Phe Ser Ile Leu Ser Asp Ala  
693 115 120 125  
E--> 695 gat atg ccg gaa gtg tcg gac cgc gac aga att tcg atg att tct gaa  
696 432  
698 Asp Met Pro Glu Val Ser Asp Arg Asp Arg Ile Ser Met Ile Ser Glu  
699 130 135 140  
E--> 701 ctg cgc agc gcc agt ggt att gcc gga atg tgc ggt ggt cag gca tta  
702 480  
704 Leu Ala Ser Ala Ser Gly Ile Ala Gly Met Cys Gly Gly Gln Ala Leu  
705 145 150 155 160  
E--> 707 gat tta gac gcg gaa ggc aaa cac gta cct ctg gac gcg ctt gag cgt  
708 528  
710 Asp Leu Asp Ala Glu Gly Lys His Val Pro Leu Asp Ala Leu Glu Arg  
711 165 170 175  
E--> 713 att cat cgt cat aaa acc ggc gca ttg att cgc gcc gcc gtt cgc ctt  
714 576  
716 Ile His Arg His Lys Thr Gly Ala Leu Ile Arg Ala Ala Val Arg Leu  
717 180 185 190  
E--> 719 ggt gca tta agc gcc gga gat aaa gga cgt cgt gtc ctg ccg gta ctc  
720 624  
722 Gly Ala Leu Ser Ala Gly Asp Lys Gly Arg Arg Ala Leu Pro Val Leu

*James*

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723 195 200 205  
E--> 725 gac aag tat gca gag agc atc ggc ctt gcc ttc cag gtt cag gat gac  
726 672  
728 Asp Lys Tyr Ala Glu Ser Ile Gly Leu Ala Phe Gln Val Gln Asp Asp  
729 210 215 220  
E--> 731 atc ctg gat gtg gtg gga gat act gca acg ttg gga aaa cgc cag ggt  
732 720  
734 Ile Leu Asp Val Val Gly Asp Thr Ala Thr Leu Gly Lys Arg Gln Gly  
735 225 230 235 240  
E--> 737 gcc gac cag caa ctt ggt aaa agt acc tac cct gca ctt ctg ggt ctt  
738 768  
740 Ala Asp Gln Gln Leu Gly Lys Ser Thr Tyr Pro Ala Leu Leu Gly Leu  
741 245 250 255  
E--> 743 gag caa gcc cggt aag aaa gcc cggt gat ctg atc gac gat gcc cgt cag  
744 816  
746 Glu Gln Ala Arg Lys Lys Ala Arg Asp Leu Ile Asp Asp Ala Arg Gln  
747 260 265 270  
E--> 749 tcg ctg aaa caa ctg gct gaa cag tca ctc gat acc tcg gca ctg gaa  
750 864  
752 Ser Leu Lys Gln Leu Ala Glu Gln Ser Leu Asp Thr Ser Ala Leu Glu  
753 275 280 285  
E--> 755 gcg cta gcg gac tac atc atc cag cgt aat aaa  
756 897  
758 Ala Leu Ala Asp Tyr Ile Ile Gln Arg Asn Lys  
759 290 295  
762 <210> SEQ ID NO: 8  
763 <211> LENGTH: 240  
764 <212> TYPE: DNA  
765 <213> ORGANISM: Escherichia coli  
767 <220> FEATURE:  
768 <221> NAME/KEY: CDS  
769 <222> LOCATION: (1)..(240)  
771 <400> SEQUENCE: 8  
E--> 772 atg ccg aag aaa aat gag gcg ccc gcc agc ttt gaa aag gcg ctg agc  
773 48  
775 Met Pro Lys Lys Asn Glu Ala Pro Ala Ser Phe Glu Lys Ala Leu Ser  
776 1 5 10 15  
E--> 778 gag ctg gaa cag att gta acc cgt ctg gaa agt ggc gac ctg ccg ctg  
779 96  
781 Glu Leu Glu Gln Ile Val Thr Arg Leu Glu Ser Gly Asp Leu Pro Leu  
782 20 25 30  
E--> 784 gaa gag gcg ctg aac gag ttc gaa cgc ggc gtg cag ctg gca cgt cag  
785 144  
787 Glu Glu Ala Leu Asn Glu Phe Glu Arg Gly Val Gln Leu Ala Arg Gln  
788 35 40 45  
E--> 790 ggg cag gcc aaa tta caa caa gcc gaa cag cgc gta caa att ctg ctg  
791 192  
793 Gly Gln Ala Lys Leu Gln Gln Ala Glu Gln Arg Val Gln Ile Leu Leu  
794 50 55 60

*Dame*

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Input Set : A:\1241.16 sequence.txt  
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E--> 796 tct gac aat gaa gac gcc tct cta acc cct ttt aca ccg gac aat gag  
 797 240  
 799 Ser Asp Asn Glu Asp Ala Ser Leu Thr Pro Phe Thr Pro Asp Asn Glu  
 800 65 70 75 80  
 803 <210> SEQ ID NO: 9  
 804 <211> LENGTH: 1044  
 805 <212> TYPE: DNA  
 806 <213> ORGANISM: Escherichia coli  
 808 <220> FEATURE:  
 809 <221> NAME/KEY: CDS  
 810 <222> LOCATION: (1)..(1044)  
 812 <400> SEQUENCE: 9  
 E--> 813 gtg act ggg gtg aac gaa tgc agc cgc agc aca tgc aac ttg aag tat  
 814 48  
 816 Val Thr Gly Val Asn Glu Cys Ser Arg Ser Thr Cys Asn Leu Lys Tyr  
 817 1 5 10 15  
 E--> 819 gac gag tat agc agg agt ggc agc atg caa tac aac ccc tta gga aaa  
 820 96  
 822 Asp Glu Tyr Ser Arg Ser Gly Ser Met Gln Tyr Asn Pro Leu Gly Lys  
 823 20 25 30  
 E--> 825 acc gac ctt cgc gtt tcc cga ctt tgc ctc ggc tgt atg acc ttt ggc  
 826 144  
 828 Thr Asp Leu Arg Val Ser Arg Leu Cys Leu Gly Cys Met Thr Phe Gly  
 829 35 40 45  
 E--> 831 gag cca gat cgc ggt aat cac gca tgg aca ctg ccg gaa gaa agc agc  
 832 192  
 834 Glu Pro Asp Arg Gly Asn His Ala Trp Thr Leu Pro Glu Glu Ser Ser  
 835 50 55 60  
 E--> 837 cgt ccc ata att aaa cgt gca ctg gaa ggc ggc ata aat ttc ttt gat  
 838 240  
 840 Arg Pro Ile Ile Lys Arg Ala Leu Glu Gly Ile Asn Phe Phe Asp  
 841 65 70 75 80  
 E--> 843 acc gcc aac agt tat tct gac ggc agc agc gaa gag atc gtc ggt cgc  
 844 288  
 846 Thr Ala Asn Ser Tyr Ser Asp Gly Ser Ser Glu Glu Ile Val Gly Arg  
 847 85 90 95  
 E--> 849 gca ctg cgg gat ttc gcc cgt cgt gaa gac gtg gtc gtt gcg acc aaa  
 850 336  
 852 Ala Leu Arg Asp Phe Ala Arg Arg Glu Asp Val Val Ala Thr Lys  
 853 100 105 110  
 E--> 855 gtg ttc cat cgc gtt ggt gat tta ccg gaa gga tta tcc cgt gcg caa  
 856 384  
 858 Val Phe His Arg Val Gly Asp Leu Pro Glu Gly Leu Ser Arg Ala Gln  
 859 115 120 125  
 E--> 861 att ttg cgc tct atc gac gac agc ctg cga cgt ctc ggc atg gat tat  
 862 432  
 864 Ile Leu Arg Ser Ile Asp Asp Ser Leu Arg Arg Leu Gly Met Asp Tyr  
 865 130 135 140  
 E--> 867 gtc gat atc ctg caa att cat cgc tgg gat tac aac acg ccg atc gaa

*Dawn*

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868 480  
870 Val Asp Ile Leu Gln Ile His Arg Trp Asp Tyr Asn Thr Pro Ile Glu  
871 145 150 155 160  
E--> 873 gag acg ctg gaa gcc ctc aac gac gtg gta aaa gcc ggg aaa gcg cgt  
874 528  
875 Glu Thr Leu Glu Ala Leu Asn Asp Val Val Lys Ala Gly Lys Ala Arg  
877 165 170 175  
E--> 879 tat atc ggc gcg tca tca atg cac gct tcg cag ttt gct cag gca ctg  
880 576  
882 Tyr Ile Gly Ala Ser Ser Met His Ala Ser Gln Phe Ala Gln Ala Leu  
883 180 185 190  
E--> 885 gaa ctc caa aaa cag cac ggc tgg gcg cag ttt gtc agt atg cag gat  
886 624  
888 Glu Leu Gln Lys Gln His Gly Trp Ala Gln Phe Val Ser Met Gln Asp  
889 195 200 205  
E--> 891 cac tac aat ctg att tat cgt gaa gaa gag cgc gag atg cta cca ctg  
892 672  
894 His Tyr Asn Leu Ile Tyr Arg Glu Glu Arg Glu Met Leu Pro Leu  
895 210 215 220  
E--> 897 tgt tat cag gag ggc gtg gcg gta att cca tgg agc ccg ctg gca agg  
898 720  
900 Cys Tyr Gln Glu Gly Val Ala Val Ile Pro Trp Ser Pro Leu Ala Arg  
901 225 230 235 240  
E--> 903 ggc cgt ctg acg cgt ccg tgg gga gaa act acc gca cga ctg gtg tct  
904 768  
906 Gly Arg Leu Thr Arg Pro Trp Gly Glu Thr Thr Ala Arg Leu Val Ser  
907 245 250 255  
E--> 909 gat gag gtg ggg aaa aat ctc tat aaa gaa agc gat gaa aat gac gcg  
910 816  
912 Asp Glu Val Gly Lys Asn Leu Tyr Lys Glu Ser Asp Glu Asn Asp Ala  
913 260 265 270  
E--> 915 cag atc gca gag cgg tta aca ggc gtc agt gaa gaa ctg ggg gcg aca  
916 864  
918 Gln Ile Ala Glu Arg Leu Thr Gly Val Ser Glu Glu Ala Thr  
919 275 280 285  
E--> 921 cga gca caa gtt gcg ctg gcc tgg ttg ttg agt aaa ccg ggc att gcc  
922 912  
924 Arg Ala Gln Val Ala Leu Ala Trp Leu Leu Ser Lys Pro Gly Ile Ala  
925 290 295 300  
E--> 927 gca ccg att atc gga act tcg cgc gaa gaa cag ctt gat gag cta ttg  
928 960  
930 Ala Pro Ile Ile Gly Thr Ser Arg Glu Glu Gln Leu Asp Glu Leu Leu  
931 305 310 315 320  
E--> 933 aac gcg gtg gat atc act ttg aag ccg gaa cag att gcc gaa ctg gaa  
934 1008  
936 Asn Ala Val Asp Ile Thr Leu Lys Pro Glu Gln Ile Ala Glu Leu Glu  
937 325 330 335  
E--> 939 acg ccg tat aaa ccg cat cct gtc gta gga ttt aaa  
940 1044

*Patent*

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942 Thr Pro Tyr Lys Pro His Pro Val Val Gly Phe Lys  
 943 340 345  
 946 <210> SEQ ID NO: 10  
 947 <211> LENGTH: 1194  
 948 <212> TYPE: DNA  
 949 <213> ORGANISM: Escherichia coli  
 951 <230> FEATURE:  
 952 <221> NAME/KEY: CDS  
 953 <222> LOCATION: (1)..(1194)  
 955 <400> SEQUENCE: 10  
 E--> 956 atg aag caa ctc acc att ctg ggc tcg acc ggc tcg att ggt tgc agc  
 957 48  
 959 Met Lys Gln Leu Thr Ile Leu Gly Ser Thr Gly Ser Ile Gly Cys Ser  
 960 1 5 10 15  
 E--> 962 acg ctg gac gtg gtg cgc cat aat ccc gaa cac ttc cgc gta gtt gcg  
 963 96  
 965 Thr Leu Asp Val Val Arg His Asn Pro Glu His Phe Arg Val Val Ala  
 966 20 25 30  
 E--> 968 ctg gtg gca ggc aaa aat gtc act cgc atg gta gaa cag tgc ctg gaa  
 969 144  
 971 Leu Val Ala Gly Lys Asn Val Thr Arg Met Val Glu Gln Cys Leu Glu  
 972 35 40 45  
 E--> 974 ttc tct ccc cgc tat gcc gta atg gac gat gaa gcg agt gcg aaa ctt  
 975 192  
 977 Phe Ser Pro Arg Tyr Ala Val Met Asp Asp Glu Ala Ser Ala Lys Leu  
 978 50 55 60  
 E--> 980 ctt aaa acg atg cta cag caa cag ggt agc cgc acc gaa gtc tta agt  
 981 240  
 983 Leu Lys Thr Met Leu Gln Gln Gly Ser Arg Thr Glu Val Leu Ser  
 984 65 70 75 80  
 E--> 986 ggg caa caa gcc gct tgc gat atg gca gcg ctt gag gat gtt gat cag  
 987 288  
 989 Gly Gln Ala Ala Cys Asp Met Ala Ala Leu Glu Asp Val Asp Gln  
 990 85 90 95  
 E--> 992 gtg atg gca gcc att gtt ggc gct gct ggg ctg tta cct acg ctt gct  
 993 336  
 995 Val Met Ala Ala Ile Val Gly Ala Ala Gly Leu Leu Pro Thr Leu Ala  
 996 100 105 110  
 E--> 998 gcg atc cgc gcg ggt aaa acc att ttg ctg gcc aat aaa gaa tca ctg  
 999 384  
 1001 Ala Ile Arg Ala Gly Lys Thr Ile Leu Leu Ala Asn Lys Glu Ser Leu  
 1002 115 120 125  
 E--> 1004 gtt acc tgc gga cgt ctg ttt atg gac gcc gta aag cag agc aaa gcg  
 1005 432  
 1007 Val Thr Cys Gly Arg Leu Phe Met Asp Ala Val Lys Gln Ser Lys Ala  
 1008 130 135 140  
 E--> 1010 caa ttg tta ccg gtc gat agc gaa cat aac gcc att ttt cag agt tta  
 1011 480  
 1013 Gln Leu Leu Pro Val Asp Ser Glu His Asn Ala Ile Phe Gln Ser Leu

*Danne*

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Input Set : A:\1241.16 sequence.txt  
Output Set: N:\CRF3\12262000\I673198.raw

1014 145 150 155 160  
E--> 1016 ccg caa cct atc cag cat aat ctg gga tac gct gac ctt gag caa aat  
1017 528  
1019 Pro Gln Pro Ile Gln His Asn Leu Gly Tyr Ala Asp Leu Glu Gln Asn  
1020 165 170 175  
E--> 1022 ggc gtg gtg tcc att tta ctt acc ggg tct ggt ggc cct ttc cgt gag  
1023 576  
1025 Gly Val Val Ser Ile Leu Leu Thr Gly Ser Gly Gly Pro Phe Arg Glu  
1026 180 185 190  
E--> 1028 acg cca ttg cgc gat ttg gca aca atg acg ccg gat caa gcc tgc cgt  
1029 624  
1031 Thr Pro Leu Arg Asp Leu Ala Thr Met Thr Pro Asp Gln Ala Cys Arg  
1032 195 200 205  
E--> 1034 cat ccg aac tgg tcg atg ggg cgt aaa att tct gtc gat tcg gct acc  
1035 672  
1037 His Pro Asn Trp Ser Met Gly Arg Lys Ile Ser Val Asp Ser Ala Thr  
1038 210 215 220  
E--> 1040 atg atg aac aaa ggt ctg gaa tac att gaa gcg cgt tgg ctg ttt aac  
1041 720  
1043 Met Met Asn Lys Gly Leu Glu Tyr Ile Glu Ala Arg Trp Leu Phe Asn  
1044 225 230 235 240  
E--> 1046 gcc agc gcc agc cag atg gaa gtg ctg att cac ccg cag tca gtg att  
1047 768  
1049 Ala Ser Ala Ser Gln Met Glu Val Leu Ile His Pro Gln Ser Val Ile  
1050 245 250 255  
E--> 1052 cac tca atg gtg cgc tat cag gac ggc agt gtt ctg gcg cag ctg ggg  
1053 816  
1054 His Ser Met Val Arg Tyr Gln Asp Gly Ser Val Leu Ala Gln Leu Gly  
1055 260 265 270  
E--> 1057 gaa ccg gat atg gta cgc caa ttg ccc aca cca tgg gca tgg ccg aat  
1058 864  
1060 Glu Pro Asp Met Val Arg Gln Leu Pro Thr Pro Trp Ala Trp Pro Asn  
1061 275 280 285  
E--> 1063 cgc gtg aac tct ggc gtg aag ccg ctc gat ttt tgc aaa cta agt gcg  
1064 912  
1066 Arg Val Asn Ser Gly Val Lys Pro Leu Asp Phe Cys Lys Leu Ser Ala  
1067 290 295 300  
E--> 1069 ttg aca ttt gcc gca ccg gat tat gat cgt tat cca tgc ctg aaa ctg  
1070 960  
1072 Leu Thr Phe Ala Ala Pro Asp Tyr Asp Arg Tyr Pro Cys Leu Lys Leu  
1073 305 310 315 320  
E--> 1075 gcg atg gag gcg ttc gaa caa ggc cag gca gcg acg aca gca ttg aat  
1076 1008  
1078 Ala Met Glu Ala Phe Glu Gln Gly Gln Ala Ala Thr Thr Ala Leu Asn  
1079 325 330 335  
E--> 1081 gcc gca aac gaa atc acc gtt gct gct ttt ctt gcg caa caa atc cgc  
1082 1056  
1084 Ala Ala Asn Glu Ile Thr Val Ala Ala Phe Leu Ala Gln Gln Ile Arg  
1085 340 345 350

*Dame*

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Input Set : A:\1241.16 sequence.txt  
 Output Set: N:\CRF3\12262000\I673198.raw

E--> 1087 ttt acg gat atc gct gcg ttg aat tta tcc gta ctg gaa aaa atg gat  
 1088 1104  
 1090 Phe Thr Asp Ile Ala Ala Leu Asn Leu Ser Val Leu Glu Lys Met Asp  
 1091 355 360 365  
 E--> 1093 atg cgc gaa cca caa tgt gtg gac gat gtg tta tct gtt gat gcg aac  
 1094 1152  
 1096 Met Arg Glu Pro Gln Cys Val Asp Asp Val Leu Ser Val Asp Ala Asn  
 1097 370 375 380  
 E--> 1099 gcg cgt gaa gtc gcc aga aaa gag gtg atg cgt ctc gca agc  
 1100 1194  
 1102 Ala Arg Glu Val Ala Arg Lys Glu Val Met Arg Leu Ala Ser  
 1103 385 390 395  
 1106 <210> SEQ ID NO: 11  
 1107 <211> LENGTH: 4390  
 1108 <212> TYPE: DNA  
 1109 <213> ORGANISM: Escherichia coli  
 1111 <220> FEATURE:  
 1112 <221> NAME/KEY: CDS  
 1113 <222> LOCATION: (208)..(447)  
 1115 <220> FEATURE:  
 1116 <221> NAME/KEY: CDS  
 1117 <222> LOCATION: (450)..(1346)  
 1119 <220> FEATURE:  
 1120 <221> NAME/KEY: CDS  
 1121 <222> LOCATION: (1374)..(3233)  
 1123 <220> FEATURE:  
 1124 <221> NAME/KEY: CDS  
 1125 <222> LOCATION: (3344)..(4390)  
 1127 <400> SEQUENCE: 11  
 E--> 1128 atggcggcaa tggtcgttg gcaaggctta agcgacttgt atagggaaaa atacagcagc  
 1129 60  
 E--> 1132 ccacacctgc ggctgcattcc aggcgcggaa gtataccact aacatcgctt tgctgtcac  
 1133 120  
 E--> 1136 atcaccttac cattgcgcgt tatttgctat ttgccttag tccgttacca tgacggggcg  
 1137 180  
 E--> 1140 aaaaatattt agagtccagac attcatt atg ccg aag aaa aat gag gcg ccc gcc  
 1141 234  
 1143 Met Pro Lys Lys Asn Glu Ala Pro Ala  
 1144 1 5  
 E--> 1146 agc ttt gaa aag gcg ctg agc gag ctg gaa cag att gta acc cgt ctg  
 1147 282  
 1149 Ser Phe Glu Lys Ala Leu Ser Glu Leu Glu Glu Ile Val Thr Arg Leu  
 1150 10 15 20 25  
 E--> 1152 gaa agt ggc gac ctg ccg ctg gaa gag gcg ctg aac gag ttc gaa cgc  
 1153 330  
 1155 Glu Ser Gly Asp Leu Pro Leu Glu Glu Ala Leu Asn Glu Phe Glu Arg  
 1156 30 35 40  
 E--> 1158 ggc gtg cag ctg gca cgt cag ggg cag gcc aaa tta caa caa gcc gaa  
 1159 378

*Same*

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Input Set : A:\1241.16\sequence.txt  
Output Set: N:\CRF3\12262000\I673198.raw

1161 Gly Val Gln Leu Ala Arg Gln Gly Gln Ala Lys Leu Gln Gln Ala Glu  
1162 45 50 55  
E--> 1164 cag cgc gta caa att ctg ctg tct gac aat gaa gac gcc tct cta acc  
1165 426  
1167 Gln Arg Val Gln Ile Leu Leu Ser Asp Asn Glu Asp Ala Ser Leu Thr  
1168 60 65 70  
E--> 1170 cct ttt aca ccg gac aat gag ta atg gac ttt ccg cag caa ctc gaa  
1171 473  
W--> 1173 Pro Phe Thr Pro Asp Asn Glu Met Asp Phe Pro Gln Gln Leu Glu  
W--> 1174 75 80 1 5  
E--> 1176 gcc tgc gtt aag cag gcc aac cag cgc ctg agc cgt ttt atc gcc cca  
1177 521  
1179 Ala Cys Val Lys Gln Ala Asn Gln Ala Leu Ser Arg Phe Ile Ala Pro  
W--> 1180 10 15 20  
E--> 1182 ctg ccc ttt cag aac act ccc gtg gtc gaa acc atg cag tat ggc gca  
1183 569  
1185 Leu Pro Phe Gln Asn Thr Pro Val Val Glu Thr Met Gln Tyr Gly Ala  
W--> 1186 25 30 35 40  
E--> 1188 tta tta ggt ggt aag cgc ctg cga cct ttc ctg gtt tat gcc acc ggt  
1189 617  
1191 Leu Leu Gly Gly Lys Arg Leu Arg Pro Phe Leu Val Tyr Ala Thr Gly  
W--> 1192 45 50 55  
E--> 1194 cat atg ttc ggc gtt agc aca aac acg ctg gac gca ccc gct gcc gcc  
1195 665  
1197 His Met Phe Gly Val Ser Thr Asn Thr Leu Asp Ala Pro Ala Ala Ala  
W--> 1198 60 65 70  
E--> 1200 gtt gag tgg atc cac gct tac tca tta att cat gat gat tta ccg gca  
1201 713  
1203 Val Glu Cys Ile His Ala Tyr Ser Leu Ile His Asp Asp Leu Pro Ala  
W--> 1204 75 80 85  
E--> 1206 atg gat gat gac gat ctg cgt cgc ggt ttg cca acc tgc cat gtc aag  
1207 761  
1209 Met Asp Asp Asp Asp Leu Arg Arg Gly Leu Pro Thr Cys His Val Lys  
W--> 1210 90 95 100  
E--> 1212 ttt ggc gaa gca aac gcg att ctc gct ggc gac gct tta caa acg ctg  
1213 809  
1215 Phe Gly Glu Ala Asn Ala Ile Leu Ala Gly Asp Ala Leu Gln Thr Leu  
W--> 1216 105 110 115 120  
E--> 1218 gcg ttc tcg att tta agc gat gcc gat atg cgc gaa gtc tcg gac cgc  
1219 857  
1221 Ala Phe Ser Ile Leu Ser Asp Ala Asp Met Pro Glu Val Ser Asp Arg  
W--> 1222 125 130 135  
E--> 1224 gac aga att tcg atg att tct gaa ctg gcg agc gcc agt ggt att gcc  
1225 905  
1227 Asp Arg Ile Ser Met Ile Ser Glu Leu Ala Ser Ala Ser Gly Ile Ala  
W--> 1228 140 145 150  
E--> 1230 gga atg tgc ggt ggt cag gca tta gat tta gac gcg gaa ggc aaa cac  
1231 953  
1233 Gly Met Cys Gly Gly Gln Ala Leu Asp Leu Asp Ala Glu Gly Lys His

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Input Set : A:\1241.16 sequence.txt  
Output Set: N:\CRF3\12262000\1673198.raw

W--> 1234 . 155 160 165  
E--> 1236 gta cct ctg gac gcg ctt gag cgt att cat cgt cat aaa acc ggc gca  
1237 1001  
1239 Val Pro Leu Asp Ala Leu Glu Arg Ile His Arg His Lys Thr Gly Ala  
W--> 1240 170 175 180  
E--> 1242 ttg att cgc gcc gcc gtt cgc ctt ggt gca tta agc gcc gga gat aaa  
1243 1049  
1245 Leu Ile Arg Ala Ala Val Arg Leu Gly Ala Leu Ser Ala Gly Asp Lys  
W--> 1246 185 190 195 200  
E--> 1248 gga cgt cgt gct ctg ccg gta ctc gac aag tat gca gag agc atc ggc  
1249 1097  
1251 Gly Arg Arg Ala Leu Pro Val Leu Asp Lys Tyr Ala Glu Ser Ile Gly  
W--> 1252 205 210 215  
E--> 1254 ctt gcc ttc cag gtt cag gat gac atc ctg gat gtg gtg gga gat act  
1255 1145  
1257 Leu Ala Phe Gln Val Gln Asp Asp Ile Leu Asp Val Val Gly Asp Thr  
W--> 1258 220 225 230  
E--> 1260 gca acg ttg gga aaa cgc cag ggt gcc gac cag caa ctt ggt aaa agt  
1261 1193  
1263 Ala Thr Leu Gly Lys Arg Gln Gly Ala Asp Gln Gln Leu Gly Lys Ser  
W--> 1264 235 240 245  
E--> 1266 acc tac cct gca ctt ctg ggt ctt gag caa gcc cgg aag aaa gcc cgg  
1267 1241  
1269 Thr Tyr Pro Ala Leu Leu Gly Leu Glu Gln Ala Arg Lys Lys Ala Arg  
W--> 1270 250 255 260  
E--> 1272 gat ctg atc gac gat gcc cgt cag tgc ctg aaa caa ctg gct gaa cag  
1273 1289  
1275 Asp Leu Ile Asp Asp Ala Arg Gln Ser Leu Lys Gln Leu Ala Glu Gln  
W--> 1276 265 270 275 280  
E--> 1278 tca ctc gat acc tgc gca ctg gaa gcg cta gcg gac tac atc atc cag  
1279 1337  
1281 Ser Leu Asp Thr Ser Ala Leu Glu Ala Leu Ala Asp Tyr Ile Ile Gln  
W--> 1282 285 290 295  
E--> 1284 cgt aat aaa taaacaataa gtatataatg gccccctg atg agt ttt gat att gcc  
1285 1391  
1287 Arg Asn Lys Met Ser Phe Asp Ile Ala  
W--> 1288 1 5  
E--> 1290 aaa tac ccg acc ctg gca ctg gtc gac tcc acc cag gag tta cga ctg  
1291 1439  
1293 Lys Tyr Pro Thr Leu Ala Leu Val Asp Ser Thr Gln Glu Leu Arg Leu  
W--> 1294 10 15 20  
E--> 1296 ttg ccg aaa gag agt tta ccg aaa ctc tgc gac gaa ctg cgc cgc tat  
1297 1487  
1299 Leu Pro Lys Glu Ser Leu Pro Lys Leu Cys Asp Glu Leu Arg Arg Tyr  
W--> 1300 25 30 35  
E--> 1302 tta ctc gac agc gtg agc cgt tcc agc ggg cac ttc gcc tcc ggg ctg  
1303 1535  
1305 Leu Leu Asp Ser Val Ser Arg Ser Ser Gly His Phe Ala Ser Gly Leu  
W--> 1306 40 45 50

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Input Set : A:\1241.16 sequence.txt  
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E--> 1308 ggc acg gtc gaa ctg acc gtg gcg ctg cac tat gtc tac aac acc acc ccg  
1309 1583  
1311 Gly Thr Val Glu Leu Thr Val Ala Leu His Tyr Val Tyr Asn Thr Pro  
W--> 1312 55 60 65 70  
E--> 1314 ttt gac caa ttg att tgg gat gtg ggg cat cag gct tat ccg cat aaa  
1315 1631  
1317 Phe Asp Gln Leu Ile Trp Asp Val Gly His Gln Ala Tyr Pro His Lys  
W--> 1318 75 80 85  
E--> 1320 att ttg acc gga cgc cgc gac aaa atc ggc acc atc cgt cag aaa ggc  
1321 1679  
1322 Ile Leu Thr Gly Arg Arg Asp Lys Ile Gly Thr Ile Arg Gln Lys Gly  
W--> 1323 90 95 100  
E--> 1325 ggt ctg cac ccg ttc ccg tgg cgc ggc gaa agc gaa tat gac gta tta  
1326 1727  
1328 Gly Leu His Pro Phe Pro Trp Arg Gly Glu Ser Glu Tyr Asp Val Leu  
W--> 1329 105 110 115  
E--> 1331 agc gtc ggg cat tca tca acc tcc atc agt gcc gga att ggt att gcg  
1332 1775  
1334 Ser Val Gly His Ser Ser Thr Ser Ile Ser Ala Gly Ile Gly Ile Ala  
W--> 1335 120 125 130  
E--> 1337 gtt gct gcc gaa aaa gaa ggc aaa aat cgc cgc acc gtc tgt gtc att  
1338 1823  
1340 Val Ala Ala Glu Lys Glu Gly Lys Asn Arg Arg Thr Val Cys Val Ile  
W--> 1341 135 140 145 150  
E--> 1344 ggc gat ggc gcg att acc gca ggc atg gcg ttt gaa gcg atg aat cac  
1345 1871  
1347 Gly Asp Gly Ala Ile Thr Ala Gly Met Ala Phe Glu Ala Met Asn His  
W--> 1348 155 160 165  
E--> 1350 gcg ggc gat atc cgt cct gat atg ctg gtg att ctc aac gac aat gaa  
1351 1919  
1353 Ala Gly Asp Ile Arg Pro Asp Met Leu Val Ile Leu Asn Asp Asn Glu  
W--> 1354 170 175 180  
E--> 1356 atg tcg att tcc gaa aat gtc ggc gcg ctc aac aac cat ctg gca cag  
1357 1967  
1359 Met Ser Ile Ser Glu Asn Val Gly Ala Leu Asn Asn His Leu Ala Gln  
W--> 1360 185 190 195  
E--> 1362 ctg ctt tcc ggt aag ctt tac tct tca ctg cgc gaa ggc ggg aaa aaa  
1363 2015  
1365 Leu Leu Ser Gly Lys Leu Tyr Ser Ser Leu Arg Glu Gly Lys Lys  
W--> 1366 200 205 210  
E--> 1368 gtt ttc tct ggc gtg cgc cca att aaa gag ctg ctc aaa cgc acc gaa  
1369 2063  
1371 Val Phe Ser Gly Val Pro Pro Ile Lys Glu Leu Leu Lys Arg Thr Glu  
W--> 1372 215 220 225 230  
E--> 1374 gaa cat att aaa ggc atg gta gtc cct ggc acg ttg ttt gaa gag ctg  
1375 2111  
1377 Glu His Ile Lys Gly Met Val Val Pro Gly Thr Leu Phe Glu Glu Leu  
W--> 1378 235 240 245  
E--> 1380 ggc ttt aac tac atc ggc ccg gtc gac ggt cac gat gtc ctg ggg ctt

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Input Set : A:\1241.16 sequence.txt  
 Output Set: N:\CRF3\12262000\1673198.raw

1381 2159  
 1383 Gly Phe Asn Tyr Ile Gly Pro Val Asp Gly His Asp Val Leu Gly Leu  
 W--> 1384 250 255 260  
 E--> 1386 atc acc acg cta aag aac atg cgc gac ctg aaa ggc ccg cag ttc ctg  
 1387 2207  
 1389 Ile Thr Leu Lys Asn Met Arg Asp Leu Lys Gly Pro Gln Phe Leu  
 W--> 1390 265 270 275  
 E--> 1392 cat atc atg acc aaa aaa ggt cgt ggt tat gaa ccg gca gaa aaa gac  
 1393 2255  
 1395 His Ile Met Thr Lys Lys Gly Arg Gly Tyr Glu Pro Ala Glu Lys Asp  
 W--> 1396 280 285 290  
 E--> 1398 ccg atc act ttc cac gcc gtc cct aaa ttt gat ccc tcc agc ggt tgt  
 1399 2303  
 1401 Pro Ile Thr Phe His Ala Val Pro Lys Phe Asp Pro Ser Ser Gly Cys  
 W--> 1402 295 300 305 310  
 E--> 1404 ttg ccg aaa agt agc ggc ggt ttg ccg agc tat tca aaa atc ttt ggc  
 1405 2351  
 1407 Leu Pro Lys Ser Ser Gly Gly Leu Pro Ser Tyr Ser Lys Ile Phe Gly  
 W--> 1408 315 320 325  
 E--> 1410 gac tgg ttg tgc gaa acg gca gcg aaa gac aac aag ctg atg gcg att  
 1411 2399  
 1413 Asp Trp Leu Cys Glu Thr Ala Ala Lys Asp Asn Lys Leu Met Ala Ile  
 W--> 1414 330 335 340  
 E--> 1416 act ccg gcg atg cgt gaa ggt tcc ggc atg gtc gag ttt tca cgt aaa  
 1417 2447  
 1419 Thr Pro Ala Met Arg Glu Gly Ser Gly Met Val Glu Phe Ser Arg Lys  
 W--> 1420 345 350 355  
 E--> 1422 ttc ccg gat cgc tac ttc gac gtc gca att gcc gag caa cac gcg gtc  
 1423 2495  
 1425 Phe Pro Asp Arg Tyr Phe Asp Val Ala Ile Ala Glu Gln His Ala Val  
 W--> 1426 360 365 370  
 E--> 1428 acc ttt gct gcg ggt ctg gcg att ggt ggg tac aaa ccc att gtc gcg  
 1429 2543  
 1431 Thr Phe Ala Ala Gly Leu Ala Ile Gly Gly Tyr Lys Pro Ile Val Ala  
 W--> 1432 375 380 385 390  
 E--> 1434 att tac tcc act ttc ctg caa cgc gcc tat gat cag gtc ctg cat gac  
 1435 2591  
 1437 Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp Gln Val Leu His Asp  
 W--> 1438 395 400 405  
 E--> 1440 gtc gcg att caa aag ctt ccc gtc ctg ttc gcc atc gac cgc gcg ggc  
 1441 2639  
 1443 Val Ala Ile Gln Lys Leu Pro Val Leu Phe Ala Ile Asp Arg Ala Gly  
 W--> 1444 410 415 420  
 E--> 1446 att gtt ggt gct gac ggt caa acc cat cag ggt gct ttt gat ctc tct  
 1447 2687  
 1449 Ile Val Gly Ala Asp Gly Gln Thr His Gln Gly Ala Phe Asp Leu Ser  
 W--> 1450 425 430 435  
 E--> 1452 tac ctg cgc tgc ata ccg gaa atg gtc att atg acc ccg agc gat gaa  
 1453 2735

*Sample*

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Input Set : A:\1241.16 sequence.txt  
 Output Set: N:\CRF3\12262000\I673198.raw

1455 Tyr Leu Arg Cys Ile Pro Glu Met Val Ile Met Thr Pro Ser Asp Glu  
 W--> 1456 440 445 450  
 E--> 1458 aac gaa tgt cgc cag atg ctc tat acc ggc tat cac tat aac gat ggc  
 1459 2783  
 1461 Asn Glu Cys Arg Gin Met Leu Tyr Thr Gly Tyr His Tyr Asn Asp Gly  
 W--> 1462 455 460 465 470  
 E--> 1464 ccg tca gcg gtg cgc tac ccg cgt ggc aac gcg gtc ggc gtg gaa ctg  
 1465 2831  
 1467 Pro Ser Ala Val Arg Tyr Pro Arg Gly Asn Ala Val Gly Val Glu Leu  
 W--> 1468 475 480 485  
 E--> 1470 acg ccg ctg gaa aaa cta cca att ggc aaa ggc att gtg aag cgt cgt  
 1471 2879  
 1473 Thr Pro Leu Glu Lys Leu Pro Ile Gly Lys Gly Ile Val Lys Arg Arg  
 W--> 1474 490 495 500  
 E--> 1476 ggc gag aaa ctg gcg atc ctt aac ttt ggt acg ctg atg cca gaa gcg  
 1477 2927  
 1479 Gly Glu Lys Leu Ala Ile Leu Asn Phe Gly Thr Leu Met Pro Glu Ala  
 W--> 1480 505 510 515  
 E--> 1482 gcg aaa gtc gcc gaa tcg ctg aac gcc acg ctg gtc gat atg cgt ttt  
 1483 2975  
 1485 Ala Lys Val Ala Glu Ser Leu Asn Ala Thr Leu Val Asp Met Arg Phe  
 W--> 1486 520 525 530  
 E--> 1488 gtg aaa ccg ctt gat gaa gcg tta att ctg gaa atg gcc gcc agc cat  
 1489 3023  
 1491 Val Lys Pro Leu Asp Glu Ala Leu Ile Leu Glu Met Ala Ala Ser His  
 W--> 1492 535 540 545 550  
 E--> 1494 gaa gcg ctg gtc acc gta gaa gaa aac gcc att atg ggc ggc gca ggc  
 1495 3071  
 1497 Glu Ala Leu Val Thr Val Glu Glu Asn Ala Ile Met Gly Gly Ala Gly  
 W--> 1498 555 560 565  
 E--> 1500 agc ggc gtg aac gaa gtg ctg atg gcc cat cgt aaa cca gta ccc gtg  
 1501 3119  
 1503 Ser Gly Val Asn Glu Val Leu Met Ala His Arg Lys Pro Val Pro Val  
 W--> 1504 570 575 580  
 E--> 1506 ctg aac att ggc ctg ccg gac ttc ttt att ccg caa gga act cag gaa  
 1507 3167  
 1509 Leu Asn Ile Gly Leu Pro Asp Phe Phe Ile Pro Gln Gly Thr Gln Glu  
 W--> 1510 585 590 595  
 E--> 1512 gaa atg cgc gcc gaa ctc ggc ctc gat gcc gct ggt atg gaa gcc aaa  
 1513 3215  
 1515 Glu Met Arg Ala Glu Leu Gly Leu Asp Ala Ala Gly Met Glu Ala Lys  
 W--> 1516 600 605 610  
 E--> 1518 atc aag gcc tgg ctg gca taatccctac tccactcctg ctatgcttaa  
 1519 3263  
 1521 Ile Lys Ala Trp Leu Ala  
 W--> 1522 615 620  
 E--> 1524 gaaattatttc atagactcta aataattcga gttgcaggaa ggccggcaaac gagtgaagcc  
 1525 3323  
 E--> 1528 ccagggagttt acataagtaa gtg act ggg gtg aac tgc agc cgc agc aca

*Marie*

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Input Set : A:\1241.16 sequence.txt  
 Output Set: N:\CRF3\12262000\I673198.raw

1529 3376  
 1531 Val Thr Gly Val Asn Glu Cys Ser Arg Ser Thr  
 W--> 1532 1 5 10  
 E--> 1534 tgc aac ttg aag tat gac gag tat agc agg agt ggc agc atg caa tac  
 1535 3424  
 1537 Cys Asn Leu Lys Tyr Asp Glu Tyr Ser Arg Ser Gly Ser Met Gln Tyr  
 W--> 1538 15 20 25  
 E--> 1540 aac ccc tta gga aaa acc gac ctt cgc gtt tcc cga ctt tgc ctc ggc  
 1541 3472  
 1543 Asn Pro Leu Gly Lys Thr Asp Leu Arg Val Ser Arg Leu Cys Leu Gly  
 W--> 1544 30 35 40  
 E--> 1546 tgt atg acc ttt ggc gag cca gat cgc ggt aat cac gca tgg aca ctg  
 1547 3520  
 1549 Cys Met Thr Phe Gly Glu Pro Asp Arg Gly Asn His Ala Trp Thr Leu  
 W--> 1550 45 50 55  
 E--> 1552 ccg gaa gaa agc agc cgt ccc ata att aaa cgt gca ctg gaa ggc ggc  
 1553 3568  
 1555 Pro Glu Glu Ser Ser Arg Pro Ile Ile Lys Arg Ala Leu Glu Gly  
 W--> 1556 60 65 70 75  
 E--> 1558 ata aat ttc ttt gat acc gcc aac agt tat tct gac ggc agc agc gaa  
 1559 3616  
 1561 Ile Asn Phe Phe Asp Thr Ala Asn Ser Tyr Ser Asp Gly Ser Ser Glu  
 W--> 1562 80 85 90  
 E--> 1564 gag atc gtc ggt cgc gca ctg cgg gat ttc gcc cgt cgt gaa gac gtc  
 1565 3664  
 1567 Glu Ile Val Gly Arg Ala Leu Arg Asp Phe Ala Arg Arg Glu Asp Val  
 W--> 1568 95 100 105  
 E--> 1570 gtc gtt gcg acc aaa gtg ttc cat cgc gtt ggt gat tta ccg gaa gga  
 1571 3712  
 1573 Val Val Ala Thr Lys Val Phe His Arg Val Gly Asp Leu Pro Glu Gly  
 W--> 1574 110 115 120  
 E--> 1575 tta tcc cgt gcg caa att ttg cgc tct atc gac gac agc ctg cga cgt  
 1576 3760  
 1578 Leu Ser Arg Ala Gln Ile Leu Arg Ser Ile Asp Asp Ser Leu Arg Arg  
 W--> 1579 125 130 135  
 E--> 1581 ctc ggc atg gat tat gtc gat atc ctg caa att cat cgc tgg gat tac  
 1582 3808  
 1584 Leu Gly Met Asp Tyr Val Asp Ile Leu Gln Ile His Arg Trp Asp Tyr  
 W--> 1585 140 145 150 155  
 E--> 1587 aac acg ccg atc gaa gag acg ctg gaa gcc ctc aac gac gtc gta aaa  
 1588 3856  
 1590 Asn Thr Pro Ile Glu Glu Thr Leu Glu Ala Leu Asn Asp Val Val Lys  
 W--> 1591 160 165 170  
 E--> 1593 gcc ggg aaa gcg cgt tat atc ggc gcg tca tca atg cac gct tcg cag  
 1594 3904  
 1596 Ala Gly Lys Ala Arg Tyr Ile Gly Ala Ser Ser Met His Ala Ser Gln  
 W--> 1597 175 180 185  
 E--> 1599 ttt gct cag gca ctg gaa ctc caa aaa cag cac gac ggc tgg gcg cag ttt  
 1600 3952

*same*

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Input Set : A:\1241.16 sequence.txt  
 Output Set: N:\CRF3\12262000\1673198.raw

1602 Phe Ala Gln Ala Leu Glu Leu Gln Lys Glu His Gly Trp Ala Gln Phe  
 W--> 1603 190 195 200  
 E--> 1605 gtc agt atg cag gat cac tac aat ctg att tat cgt gaa gaa gag cgc  
 1606 4000  
 1608 Val Ser Met Gln Asp His Tyr Asn Leu Ile Tyr Arg Glu Glu Glu Arg  
 W--> 1609 205 210 215  
 E--> 1611 gag atg cta cca ctg tgt tat cag gag ggc gtc gcg gta att cca tgg  
 1612 4048  
 1614 Glu Met Leu Pro Leu Cys Tyr Gln Glu Gly Val Ala Val Ile Pro Trp  
 W--> 1615 220 225 230 235  
 E--> 1617 agc ccg ctg gca agg ggc cgt ctg acg cgt ccg tgg gga gaa act acc  
 1618 4096  
 1620 Ser Pro Leu Ala Arg Gly Arg Leu Thr Arg Pro Trp Gly Glu Thr Thr  
 W--> 1621 240 245 250  
 E--> 1623 gca cga ctg gtg tct gat gag gtc ggg aaa aat ctc tat aaa gaa agc  
 1624 4144  
 1626 Ala Arg Leu Val Ser Asp Glu Val Gly Lys Asn Leu Tyr Lys Glu Ser  
 W--> 1627 255 260 265  
 E--> 1629 gat gaa aat gac gcg cag atc gca gag cgg tta aca ggc gtc agt gaa  
 1630 4192  
 1632 Asp Glu Asn Asp Ala Gln Ile Ala Glu Arg Leu Thr Gly Val Ser Glu  
 W--> 1633 270 275 280  
 E--> 1635 gaa ctg ggg gcg aca cga gca caa gtt gcg ctg gcc tgg ttg ttg agt  
 1636 4240  
 1638 Glu Leu Gly Ala Thr Arg Ala Gln Val Ala Leu Ala Trp Leu Leu Ser  
 W--> 1639 285 290 295  
 E--> 1641 aaa ccg ggc att gcc gca ccg att atc gga act tcg cgc gaa gaa cag  
 1642 4288  
 1644 Lys Pro Gly Ile Ala Ala Pro Ile Ile Gly Thr Ser Arg Glu Glu Gln  
 W--> 1645 300 305 310 315  
 E--> 1647 ctt gat gag cta ttg aac gcg gtc gat atc act ttg aag ccg gaa cag  
 1648 4336  
 1650 Leu Asp Glu Leu Leu Asn Ala Val Asp Ile Thr Leu Lys Pro Glu Gln  
 W--> 1651 320 325 330  
 E--> 1653 att gcc gaa ctg gaa acg ccg tat aaa ccg cat cct gtc gta gga ttt  
 1654 4384  
 1656 Ile Ala Glu Leu Glu Thr Pro Tyr Lys Pro His Pro Val Val Gly Phe  
 W--> 1657 335 340 345  
 E--> 1659 aaa taa  
 1660 4390  
 1662 Lys  
 1665 <210> SEQ ID NO: 12  
 1666 <211> LENGTH: 33  
 1667 <212> TYPE: DNA  
 1668 <213> ORGANISM: Artificial Sequence  
 1670 <220> FEATURE:  
 1671 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
 1673 <400> SEQUENCE: 12  
 E--> 1674 ccggatccat ggccggcaatg gttcggttggc aag

*Same*

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Input Set : A:\1241.16 sequence.txt  
Output Set: N:\CRF3\12262000\I673198.raw

1675 33  
1679 <210> SEQ ID NO: 13  
1680 <211> LENGTH: 34  
1681 <212> TYPE: DNA  
1682 <213> ORGANISM: Artificial Sequence  
1684 <220> FEATURE:  
1685 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1687 <400> SEQUENCE: 13  
E--> 1688 ccgaattctt atttaaatcc tacgacagga tgcg  
1689 34  
1693 <210> SEQ ID NO: 14  
1694 <211> LENGTH: 33  
1695 <212> TYPE: DNA  
1696 <213> ORGANISM: Artificial Sequence  
1698 <220> FEATURE:  
1699 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1701 <400> SEQUENCE: 14  
E--> 1702 ccggatccat gagttttgat attgccaaat acc  
1703 33  
1707 <210> SEQ ID NO: 15  
1708 <211> LENGTH: 33  
1709 <212> TYPE: DNA  
1710 <213> ORGANISM: Artificial Sequence  
1712 <220> FEATURE:  
1713 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1715 <400> SEQUENCE: 15  
E--> 1716 ccgaattctt atgccagcca ggcccttgatt ttg  
1717 33  
1721 <210> SEQ ID NO: 16  
1722 <211> LENGTH: 33  
1723 <212> TYPE: DNA  
1724 <213> ORGANISM: Artificial Sequence  
1726 <220> FEATURE:  
1727 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1729 <400> SEQUENCE: 16  
E--> 1730 ccgaattctt actcattgtc cgggtgaaaa ggg  
1731 33  
1735 <210> SEQ ID NO: 17  
1736 <211> LENGTH: 33  
1737 <212> TYPE: DNA  
1738 <213> ORGANISM: Artificial Sequence  
1740 <220> FEATURE:  
1741 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1743 <400> SEQUENCE: 17  
E--> 1744 ccggatccat ggactttccg cagcaactcg aag  
1745 33  
1749 <210> SEQ ID NO: 18  
1750 <211> LENGTH: 33  
1751 <212> TYPE: DNA

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Input Set : A:\1241.16 sequence.txt  
Output Set: N:\CRF3\12262000\1673198.raw

1752 <213> ORGANISM: Artificial Sequence  
1754 <220> FEATURE:  
1755 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1757 <400> SEQUENCE: 18  
E--> 1758 ccgaattctt atttattacg ctggatgtatg tag  
1759 33  
1763 <210> SEQ ID NO: 19  
1764 <211> LENGTH: 33  
1765 <212> TYPE: DNA  
1766 <213> ORGANISM: Artificial Sequence  
1768 <220> FEATURE:  
1769 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1771 <400> SEQUENCE: 19  
E--> 1772 ccggatccca atccctactc cactcctgct atg  
1773 33  
1777 <210> SEQ ID NO: 20  
1778 <211> LENGTH: 30  
1779 <212> TYPE: DNA  
1780 <213> ORGANISM: Artificial Sequence  
1782 <220> FEATURE:  
1783 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1785 <400> SEQUENCE: 20  
E--> 1786 gggggatcca agcaactcac cattctgggc  
1787 30  
1791 <210> SEQ ID NO: 21  
1792 <211> LENGTH: 30  
1793 <212> TYPE: DNA  
1794 <213> ORGANISM: Artificial Sequence  
1796 <220> FEATURE:  
1797 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1799 <400> SEQUENCE: 21  
E--> 1800 gggggatccg cttgcgagac gcatcaccc  
1801 30  
1805 <210> SEQ ID NO: 22  
1806 <211> LENGTH: 32  
1807 <212> TYPE: DNA  
1808 <213> ORGANISM: Artificial Sequence  
1810 <220> FEATURE:  
1811 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1813 <400> SEQUENCE: 22  
E--> 1814 gggggatcca gttttatat tgcggaaatacc  
1815 32  
1819 <210> SEQ ID NO: 23  
1820 <211> LENGTH: 32  
1821 <212> TYPE: DNA  
1822 <213> ORGANISM: Artificial Sequence  
1824 <220> FEATURE:  
1825 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1827 <400> SEQUENCE: 23

*Same*

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Input Set : A:\1241.16 sequence.txt  
Output Set: N:\CRF3\12262000\I673198.raw

E--> 1828 gggggatcct gccagccagg ctttgatttt gg  
1829 32  
1833 <210> SEQ TD NO: 24  
1834 <211> LENGTH: 30  
1835 <212> TYPE: DNA  
1836 <213> ORGANISM: Artificial Sequence  
1838 <220> FEATURE:  
1839 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1841 <400> SEQUENCE: 24  
E--> 1842 gggggatccg agcaactcac cattctgggc  
1843 30  
1847 <210> SEQ TD NO: 25  
1848 <211> LENGTH: 30  
1849 <212> TYPE: DNA  
1850 <213> ORGANISM: Artificial Sequence  
1852 <220> FEATURE:  
1853 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA  
1855 <400> SEQUENCE: 25  
E--> 1856 gggggatccg cttgcgagac gcatcacctc  
1857 30

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Input Set : A:\1241.16 sequence.txt  
Output Set: N:\CRF3\12262000\I673198.raw

L:9 M:201 W: Mandatory field data missing. FILE REFERENCE  
L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:402 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:6  
M:254 Repeated in SeqNo=6  
L:647 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:7  
M:254 Repeated in SeqNo=7  
L:772 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:8  
M:254 Repeated in SeqNo=8  
L:813 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:9  
M:254 Repeated in SeqNo=9  
L:956 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:10  
M:254 Repeated in SeqNo=10  
L:1128 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:11  
M:254 Repeated in SeqNo=11  
L:1173 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 11  
L:1174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1192 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1216 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1240 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1252 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1258 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1282 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1288 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1300 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1312 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1318 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1329 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1341 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1348 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1354 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1360 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11

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Input Set : A:\1241.16 sequence.txt  
Output Set: N:\CRF3\12262000\I673198.raw

L:1366 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1372 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1384 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1390 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1396 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1402 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1408 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1414 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1420 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1426 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1432 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1438 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1456 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1462 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11  
L:1674 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:12  
L:1688 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:13  
L:1702 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:14  
L:1716 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:15  
L:1730 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:16  
L:1744 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:17  
L:1758 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:18  
L:1772 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:19  
L:1786 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:20  
L:1800 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:21  
L:1814 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:22  
L:1828 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:23  
L:1842 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:24  
L:1856 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:25  
L:1997 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:27  
M:254 Repeated in SeqNo=27  
L:2338 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:29  
M:254 Repeated in SeqNo=29  
L:2636 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:48 SEQ:31  
M:251 Repeated in SeqNo=31  
L:2771 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:32  
L:2784 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:33  
L:2797 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:34